

Supplementary Table 1. Cross-Sectional Associations between Loneliness and Differentially Expressed Genes at the Baseline Timepoint.

<u>Gene Symbol</u>	<u>Loneliness parameter estimate</u> ¹	<u>Loneliness fold-difference</u> ²
Upregulated in lonely / Downregulated in non-lonely		
LOC728823	0.0594	1.0420
LOC441377	0.0563	1.0398
LOC100129650	0.0556	1.0393
LOC644928	0.0554	1.0391
LOC645979	0.0539	1.0381
LOC646753	0.0531	1.0375
RPS26L	0.0518	1.0366
SIGLEC14	0.0513	1.0362
LOC641768	0.0499	1.0352
RPS26	0.0496	1.0350
RPS26P11	0.0488	1.0344
LOC644934	0.0482	1.0340
LOC650646	0.0457	1.0322
LOC644191	0.0444	1.0313
LOC650298	0.0429	1.0302
LOC100133823	0.0421	1.0296
LOC653600	0.0408	1.0287
LOC100131971	0.0392	1.0275
RPS26P10	0.0392	1.0275
CAMP	0.0354	1.0248
LOC642073	0.0353	1.0248
DEFA3	0.0346	1.0243
DEFA1B	0.0336	1.0236
LOC728937	0.0336	1.0236
LOC100129552	0.0331	1.0232
DEFA4	0.0328	1.0230
CD24	0.0316	1.0221
LOC650263	0.0316	1.0221
DEFA1	0.0296	1.0207
LTF	0.0288	1.0202
TACSTD2	0.0278	1.0195
HLA-A29.1	0.0272	1.0190
HSPA1A	0.0272	1.0190
MYL4	0.0271	1.0190
LOC731682	0.0258	1.0180
CEACAM6	0.0251	1.0176
LOC100133565	0.0250	1.0175
CEACAM8	0.0248	1.0173
ELANE	0.0242	1.0169
CX3CR1	0.0233	1.0163
FAM118A	0.0214	1.0149
SCGB3A1	0.0214	1.0149

LOC100008589	0.0208	1.0145
GIMAP4	0.0203	1.0142
HSPH1	0.0202	1.0141
LOC441763	0.0199	1.0139
METTL13	0.0197	1.0137
PRAGMIN	0.0197	1.0137
FCGR1A	0.0195	1.0136
TNFSF10	0.0194	1.0135
DUSP6	0.0192	1.0134
CXCL10	0.0191	1.0133
EPSTI1	0.0183	1.0128
PGLYRP1	0.0181	1.0126
GBP1	0.0180	1.0126
NAGK	0.0180	1.0126
RETN	0.0180	1.0126
IRF5	0.0177	1.0123
GIMAP8	0.0175	1.0122
LOC728519	0.0175	1.0122
GPBAR1	0.0172	1.0120
MRPS31	0.0167	1.0116
ZSWIM7	0.0166	1.0116
NAPSA	0.0165	1.0115
CHST15	0.0163	1.0114
APAF1	0.0162	1.0113
LOC284648	0.0161	1.0112
MAP7D1	0.0161	1.0112
NCAPG2	0.0160	1.0112
C17orf87	0.0159	1.0111
GM2A	0.0159	1.0111
NAPSB	0.0159	1.0111
RNASE3	0.0159	1.0111
ANG	0.0158	1.0110
AIM2	0.0157	1.0109
CCR2	0.0157	1.0109
CTSG	0.0157	1.0109
ERAP2	0.0157	1.0109
RPP40	0.0155	1.0108
DHRS9	0.0154	1.0107
VPS35	0.0154	1.0107
TLR7	0.0151	1.0105
C11orf75	0.0150	1.0105
DENND2D	0.0150	1.0105
FCGR1B	0.0148	1.0103
STIP1	0.0148	1.0103
ZW10	0.0146	1.0102

Downregulated in lonely / Upregulated in non-lonely

ANKRD9	-0.0144	0.9901
LOC255167	-0.0144	0.9901
C8orf45	-0.0145	0.9900

DHRS3	-0.0145	0.9900
FLJ46309	-0.0145	0.9900
HBQ1	-0.0145	0.9900
HIST1H2BC	-0.0145	0.9900
LOC641825	-0.0145	0.9900
LOC649260	-0.0145	0.9900
OSBP2	-0.0145	0.9900
TSPAN9	-0.0145	0.9900
LOC100128288	-0.0146	0.9899
LOC100131718	-0.0147	0.9899
NAT8B	-0.0147	0.9899
NFIL3	-0.0147	0.9899
CLCF1	-0.0148	0.9898
KIR2DL1	-0.0148	0.9898
NGFRAP1	-0.0148	0.9898
PHACS	-0.0148	0.9898
C1orf55	-0.0149	0.9897
MIAT	-0.0149	0.9897
USP49	-0.0149	0.9897
C9orf89	-0.0150	0.9897
PTGS1	-0.0150	0.9897
CHST13	-0.0151	0.9896
(Unnamed gene)	-0.0151	0.9896
LOC391045	-0.0151	0.9896
RPA1	-0.0151	0.9896
XK	-0.0151	0.9896
ZNF185	-0.0152	0.9895
RNF103	-0.0153	0.9895
LOC100134331	-0.0154	0.9894
CLC	-0.0155	0.9893
LOC387882	-0.0155	0.9893
LOC653071	-0.0156	0.9892
ABCC3	-0.0157	0.9892
DPYSL4	-0.0157	0.9892
FAM175A	-0.0157	0.9892
DNAJB9	-0.0158	0.9891
HGD	-0.0158	0.9891
ITGB3	-0.0158	0.9891
METRNL	-0.0158	0.9891
C7orf41	-0.0159	0.9890
PIM3	-0.0160	0.9890
PRSS23	-0.0160	0.9890
UTS2	-0.0160	0.9890
SH3BGRL2	-0.0161	0.9889
SLC2A14	-0.0161	0.9889
TSPAN33	-0.0161	0.9889
CD9	-0.0162	0.9888
(Unnamed gene)	-0.0162	0.9888
LOC654191	-0.0162	0.9888
ZC3H12A	-0.0162	0.9888
PDLIM1	-0.0163	0.9888

CD69	-0.0164	0.9887
EBI2	-0.0164	0.9887
ENC1	-0.0164	0.9887
HIST1H1C	-0.0164	0.9887
NAMPT	-0.0164	0.9887
PDE4B	-0.0164	0.9887
CXorf20	-0.0165	0.9886
SLC2A3	-0.0165	0.9886
TSC22D1	-0.0165	0.9886
ABCA1	-0.0166	0.9886
LOC651751	-0.0166	0.9886
SOCS3	-0.0167	0.9885
MIR1974	-0.0168	0.9884
TGFBR3	-0.0168	0.9884
HIST1H3H	-0.0169	0.9884
HLA-DRB6	-0.0169	0.9884
HIST1H3F	-0.0171	0.9882
RNY3	-0.0172	0.9881
MGC13057	-0.0173	0.9881
MYL9	-0.0173	0.9881
"SEPT5"	-0.0173	0.9881
SNORA70	-0.0173	0.9881
CXCL5	-0.0174	0.9880
GP6	-0.0174	0.9880
MGC3020	-0.0175	0.9879
CTDSPL	-0.0176	0.9879
PPBP	-0.0176	0.9879
(Unnamed gene)	-0.0178	0.9877
NFIB	-0.0179	0.9877
LOC649143	-0.0181	0.9875
RRP7A	-0.0181	0.9875
GRASP	-0.0183	0.9874
HIST1H2AE	-0.0183	0.9874
PGRMC1	-0.0183	0.9874
MEIS1	-0.0184	0.9873
NRGN	-0.0184	0.9873
RGS18	-0.0185	0.9873
F13A1	-0.0186	0.9872
PELI1	-0.0186	0.9872
SMOX	-0.0186	0.9872
LOC441481	-0.0188	0.9871
LOC728715	-0.0188	0.9871
ALOX12	-0.0189	0.9870
CD83	-0.0189	0.9870
SDPR	-0.0189	0.9870
TMEM158	-0.0191	0.9868
ACRBP	-0.0192	0.9868
IGJ	-0.0192	0.9868
TMEM140	-0.0192	0.9868
PPAPDC1B	-0.0193	0.9867
SIK1	-0.0193	0.9867

CABP5	-0.0195	0.9866
GNG11	-0.0196	0.9865
LOC645381	-0.0196	0.9865
BCL3	-0.0197	0.9864
GABARAPL1	-0.0197	0.9864
SLC7A5	-0.0199	0.9863
SPARC	-0.0199	0.9863
ESAM	-0.0200	0.9862
HIST1H2BK	-0.0200	0.9862
PROS1	-0.0201	0.9862
ITGB5	-0.0203	0.9860
C20orf111	-0.0205	0.9859
LOC650557	-0.0205	0.9859
MMD	-0.0205	0.9859
BMP6	-0.0206	0.9858
HIST1H2BJ	-0.0206	0.9858
HBG1	-0.0211	0.9855
SNIP1	-0.0212	0.9854
TNFAIP3	-0.0214	0.9853
GRAP2	-0.0215	0.9852
TNFRSF21	-0.0216	0.9851
GP9	-0.0218	0.9850
S100P	-0.0219	0.9849
MPL	-0.0221	0.9848
IL8RBP	-0.0222	0.9847
THBS1	-0.0222	0.9847
LOC644423	-0.0223	0.9847
LOC649841	-0.0224	0.9846
CXCR4	-0.0225	0.9845
HBG2	-0.0227	0.9844
ITGA2B	-0.0227	0.9844
RGS1	-0.0233	0.9840
G0S2	-0.0235	0.9838
PTCRA	-0.0237	0.9837
KIR3DS1	-0.0239	0.9836
MXD1	-0.0242	0.9834
NR4A2	-0.0242	0.9834
LY6G6F	-0.0243	0.9833
VWF	-0.0243	0.9833
TREML1	-0.0248	0.9830
RYBP	-0.0249	0.9829
SPOCD1	-0.0256	0.9824
IL8	-0.0258	0.9823
HIST1H2AC	-0.0264	0.9819
HBEGF	-0.0269	0.9815
LGALS2	-0.0269	0.9815
AVPI1	-0.0271	0.9814
ACCS	-0.0273	0.9813
KIFC3	-0.0274	0.9812
AQP10	-0.0275	0.9811
(Unnamed gene)	-0.0278	0.9809

SNORD13	-0.0281	0.9807
DDIT4	-0.0282	0.9806
HLA-DRB1	-0.0282	0.9806
CLDN5	-0.0300	0.9794
CLEC1B	-0.0300	0.9794
FLJ45337	-0.0312	0.9786
PFKFB3	-0.0322	0.9779
CHURC1	-0.0323	0.9779
HLA-DRB5	-0.0352	0.9759
PDZK1IP1	-0.0364	0.9751
PVALB	-0.0406	0.9723
OSM	-0.0483	0.9671
MYOM2	-0.0495	0.9663

Notes

¹ Log-linear statistical model parameter representing loneliness effect (coded to represent change in gene expression per UCLA Loneliness scale point)

² Exponentiated parameter estimate (fold-difference in magnitude gene expression per loneliness scale point)

Supplementary Table 2. Relative differences in pre-post treatment gene expression in MBSR compared to WL.

<u>Gene Symbol</u>	<u>Loneliness parameter estimate¹</u>	<u>Loneliness fold-difference²</u>
Upregulated in MBSR / Downregulated in WL control		
LOC645979	0.7415	1.67
LOC644928	0.7379	1.67
LOC646753	0.7296	1.66
LOC100129650	0.6954	1.62
LOC728823	0.6754	1.60
G0S2	0.6114	1.53
LOC441377	0.6114	1.53
LOC100133823	0.5985	1.51
LOC641768	0.5862	1.50
LOC650298	0.5832	1.50
LOC100131971	0.5776	1.49
RPS26P10	0.5722	1.49
RPS26L	0.5689	1.48
RPS26	0.5543	1.47
LOC644191	0.5345	1.45
NAMPT	0.5265	1.44
ZC3H12A	0.5189	1.43
ALAS2	0.5140	1.43
LOC100129552	0.4981	1.41
BCL3	0.4934	1.41
MAFB	0.4840	1.40
LOC650646	0.4679	1.38
YOD1	0.4593	1.37
LOC644934	0.4560	1.37
TACSTD2	0.4496	1.37
DYNLL2	0.4493	1.37
ADM	0.4448	1.36
RPS26P11	0.4430	1.36
PIM3	0.4407	1.36
SLC25A37	0.4398	1.36
KIR3DS1	0.4359	1.35
CCL2	0.4278	1.35
EGR1	0.4194	1.34
BTG3	0.4142	1.33
CD83	0.4120	1.33
HBM	0.4092	1.33
LOC147727	0.4064	1.33
LOC644936	0.4054	1.32
PFKFB3	0.3765	1.30
CA1	0.3746	1.30

SGK1	0.3732	1.30
SLC4A1	0.3710	1.29
FASTKD5	0.3707	1.29
RNF10	0.3705	1.29
ADNP2	0.3685	1.29
LOC100132395	0.3676	1.29
LOC728937	0.3672	1.29
CLCF1	0.3660	1.29
C20orf111	0.3651	1.29
C1orf55	0.3612	1.28
LOC100129882	0.3529	1.28
AHSP	0.3487	1.27
RAD23B	0.3481	1.27
DUSP5	0.3468	1.27
C16orf87	0.3463	1.27
FAM118A	0.3449	1.27
SGK	0.3431	1.27
HBA1	0.3424	1.27
SELENBP1	0.3393	1.27
HBG2	0.3383	1.26
SLC25A39	0.3372	1.26
USP36	0.3372	1.26
SPRY2	0.3367	1.26
LOC389599	0.3336	1.26
KLF11	0.3327	1.26
FFAR2	0.3309	1.26
LOC399491	0.3297	1.26
RHOU	0.3283	1.26
ZNF256	0.3280	1.26
H3F3B	0.3254	1.25
EPB42	0.3251	1.25
RPUSD2	0.3248	1.25
LOC653778	0.3232	1.25
CLP1	0.3220	1.25

Downregulated in MBSR / Upregulated in WL control

CHCHD4	-0.3229	0.80
SFRS7	-0.3234	0.80
ABI3	-0.3258	0.80
HCP5	-0.3280	0.80
AGPAT9	-0.3293	0.80
DENND2D	-0.3309	0.80
VPS35	-0.3313	0.79
MIR1974	-0.3368	0.79
ZW10	-0.3378	0.79
FKBP5	-0.3391	0.79
NUPL2	-0.3395	0.79
CISH	-0.3399	0.79
TLR8	-0.3418	0.79
DKFZp761P0423	-0.3422	0.79

HAVCR2	-0.3430	0.79
NSUN2	-0.3436	0.79
TNFSF10	-0.3442	0.79
SLA	-0.3451	0.79
LOC284648	-0.3512	0.78
PAQR8	-0.3515	0.78
SNORD3D	-0.3516	0.78
CD55	-0.3553	0.78
MS4A7	-0.3566	0.78
LOC401233	-0.3594	0.78
CHST7	-0.3603	0.78
NAGK	-0.3620	0.78
SLC35A5	-0.3621	0.78
UTS2	-0.3636	0.78
TNFAIP8L2	-0.3640	0.78
HLA-A29.1	-0.3683	0.77
RNASE3	-0.3724	0.77
TNFRSF1A	-0.3810	0.77
FOLR3	-0.3817	0.77
RAB10	-0.3823	0.77
RGS1	-0.3830	0.77
CKS2	-0.3839	0.77
C1orf77	-0.3916	0.76
FAM43A	-0.3918	0.76
LEPROTL1	-0.3933	0.76
CD24	-0.3962	0.76
ACTA2	-0.4023	0.76
CHST15	-0.4062	0.75
MAT2A	-0.4078	0.75
LOC650263	-0.4080	0.75
DCAF7	-0.4215	0.75
HLA-DRB1	-0.4263	0.74
CCR2	-0.4270	0.74
CEACAM8	-0.4321	0.74
METTL13	-0.4340	0.74
GIMAP8	-0.4356	0.74
GADD45G	-0.4420	0.74
CX3CR1	-0.4428	0.74
DEFA4	-0.4496	0.73
ELANE	-0.4647	0.72
CEACAM6	-0.4671	0.72
PRAGMIN	-0.4797	0.72
CXCL10	-0.4801	0.72
FOSB	-0.4814	0.72
CACNA2D3	-0.4865	0.71
GIMAP4	-0.4995	0.71
C17orf44	-0.5200	0.70
HSPH1	-0.5503	0.68
GAPT	-0.6080	0.66
CAMP	-0.6170	0.65
HSPA1A	-0.7367	0.60

DEFA3	-0.7960	0.58
DEFA1B	-0.8251	0.56
DEFA1	-0.8381	0.56
LOC653600	-0.9322	0.52

Notes

¹ Log-linear statistical model parameter representing treatment condition X time interaction (coded to represent MBSR change over time - WL control change over time)

² Exponentiated parameter estimate (fold-difference in magnitude of MBSR change over time relative to WL change over time)